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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/117,246B

DATE: 04/03/2002

TIME: 10:30:14

Input Set : A:\50026.004001.SEQLIST.TXT

Output Set: N:\CRF3\04032002\I117246B.raw

#19/
K.T.
4/11Raw
Seq.
6:
listing

4 <110> APPLICANT: Ludevid, Doloros
 5 Torrent, Margarita
 6 Alvarez, Inaki
 7 Perez, Pascual
 9 <120> TITLE OF INVENTION: Amino acid-enriched plant protein
 10 reserves, particularly lysine-enriched maize gamma-zein, and
 11 plants expressing such proteins
 14 <130> FILE REFERENCE: 50062/004001
 16 <140> CURRENT APPLICATION NUMBER: 09/117,246B
 17 <141> CURRENT FILING DATE: 1998-12-03
 19 <150> PRIOR APPLICATION NUMBER: PCT/FR97/00167
 20 <151> PRIOR FILING DATE: 1997-01-28
 22 <150> PRIOR APPLICATION NUMBER: FR96/01004
 23 <151> PRIOR FILING DATE: 1996-01-29
 25 <160> NUMBER OF SEQ ID NOS: 11
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 44
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Artificial Sequence
 34 <220> FEATURE:
 35 <223> OTHER INFORMATION: based on Maize
 37 <400> SEQUENCE: 1
 38 cgatgaatt aaaccaaaggc caaagccgaa gccaaaagaa ttca 44
 40 <210> SEQ ID NO: 2
 41 <211> LENGTH: 46
 42 <212> TYPE: DNA
 43 <213> ORGANISM: Artificial Sequence
 45 <220> FEATURE:
 46 <223> OTHER INFORMATION: based on Maize
 48 <400> SEQUENCE: 2
 49 agcttgaatt cttttggctt cggctttggc tttgggttga attcat 46
 51 <210> SEQ ID NO: 3
 52 <211> LENGTH: 17
 53 <212> TYPE: PRT
 54 <213> ORGANISM: Maize
 56 <400> SEQUENCE: 3
 57 Ile Glu Phe Lys Pro Lys Pro Lys Pro Lys Glu Phe Leu Gln
 58 1 5 10 15
 59 Pro
 63 <210> SEQ ID NO: 4
 64 <211> LENGTH: 28
 65 <212> TYPE: PRT

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66 <213> ORGANISM: Maize
 68 <400> SEQUENCE: 4
 69 Ile Glu Phe Lys Pro Lys Pro Lys Pro Lys Pro Lys Glu Phe Lys Pro
 70 1 5 10 15
 71 Lys Pro Lys Pro Lys Pro Lys Glu Phe Leu Gln Pro
 72 20 25
 75 <210> SEQ ID NO: 5
 76 <211> LENGTH: 20
 77 <212> TYPE: PRT
 78 <213> ORGANISM: Maize
 80 <400> SEQUENCE: 5
 81 Asp Gly Ile Asp Glu Phe Lys Pro Lys Pro Lys Pro Lys Pro Lys Glu
 82 1 5 10 15
 83 Phe Lys Leu Asp
 84 20
 87 <210> SEQ ID NO: 6
 88 <211> LENGTH: 672
 89 <212> TYPE: DNA
 90 <213> ORGANISM: Maize
 92 <220> FEATURE:
 93 <221> NAME/KEY: CDS
 94 <222> LOCATION: (1)...(672)
 96 <400> SEQUENCE: 6
 97 atg agg gtg ttg ctc gtt gcc ctc gct ctc ctg gct ctc gct gcg agc 48
 98 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Ala Ser
 99 1 5 10 15
 101 gcc acc tcc acg cat aca agc ggc ggc tgc ggc tgc cag cca ccg ccg 96
 102 Ala Thr Ser Thr His Thr Ser Gly Gly Cys Gly Cys Gln Pro Pro Pro
 103 20 25 30
 105 ccg gtt cat cta ccg ccg ccg gtg cat ctg cca cct ccg gtt cac ctg 144
 106 Pro Val His Leu Pro Pro Val His Leu Pro Pro Pro Val His Leu
 107 35 40 45
 109 cca cct ccg gtg cat ctc cca ccg ccg gtc cac ctg ccg ccg gtc 192
 110 Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val
 111 50 55 60
 113 cac ctg cca ccg gtc cat gtg ccg ccg gtt cat ctg ccg ccg 240
 114 His Leu Pro Pro Val His Val Pro Pro Pro Val His Leu Pro Pro
 115 65 70 75 80
 117 cca cca tgc cac tac cct act caa ccg ccc ccg cct cag cct cat ccc 288
 118 Pro Pro Cys His Tyr Pro Thr Gln Pro Pro Arg Pro Gln Pro His Pro
 119 85 90 95
 121 cag cca cac cca tgc ccg tgc caa cag ccg cat cca agc ccg tgc cag 336
 122 Gln Pro His Pro Cys Pro Cys Gln Gln Pro His Pro Ser Pro Cys Gln
 123 100 105 110
 125 ctg cag gga acc tgc ggc gtt ggc agc acc ccg atc ctg ggc cag tgc 384
 126 Leu Gln Gly Thr Cys Gly Val Gly Ser Thr Pro Ile Leu Gly Gln Cys
 127 115 120 125
 129 gtc gag ttt ctg agg cat cag tgc agc ccg acg gcg acg ccc tac tgc 432
 130 Val Glu Phe Leu Arg His Gln Cys Ser Pro Thr Ala Thr Pro Tyr Cys

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131	130	135	140	
133	tcg cct cag tgc cag tcg ttg cgg cag cag tgt tgc cag cag ctc agg			480
134	Ser Pro Gln Cys Gln Ser Leu Arg Gln Gln Cys Cys Gln Gln Leu Arg			
135	145	150	155	160
137	cag gtg gag ccg cag cac cgg tac cag gcg atc ttc ggc ttg gtc ctc			528
138	Gln Val Glu Pro Gln His Arg Tyr Gln Ala Ile Phe Gly Leu Val Leu			
139	165	170	175	
141	cag tcc atc ctg cag cag ccc			576
142	Gln Ser Ile Leu Gln Gln Pro Gln Ser Gly Gln Val Ala Gly Leu			
143	180	185	190	
145	ttg gcg gcg cag ata gcg cag caa ctg acg gcg atg tgc ggc ctg cag			624
146	Leu Ala Ala Gln Ile Ala Gln Gln Leu Thr Ala Met Cys Gly Leu Gln			
147	195	200	205	
149	cag ccg act cca tgc ccc tac gct gct gcc ggc ggt gtc ccc cac tga			672
150	Gln Pro Thr Pro Cys Pro Tyr Ala Ala Ala Gly Gly Val Pro His *			
151	210	215	220	
155	<210> SEQ ID NO: 7			
156	<211> LENGTH: 223			
157	<212> TYPE: PRT			
158	<213> ORGANISM: Maize			
160	<400> SEQUENCE: 7			
161	Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser			
162	1	5	10	15
163	Ala Thr Ser Thr His Thr Ser Gly Gly Cys Gly Cys Gln Pro Pro Pro			
164	20	25	30	
165	Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu			
166	35	40	45	
167	Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val			
168	50	55	60	
169	His Leu Pro Pro Pro Val His Val Pro Pro Pro Val His Leu Pro Pro			
170	65	70	75	80
171	Pro Pro Cys His Tyr Pro Thr Gln Pro Pro Arg Pro Gln Pro His Pro			
172	85	90	95	
173	Gln Pro His Pro Cys Pro Cys Gln Gln Pro His Pro Ser Pro Cys Gln			
174	100	105	110	
175	Leu Gln Gly Thr Cys Gly Val Gly Ser Thr Pro Ile Leu Gly Gln Cys			
176	115	120	125	
177	Val Glu Phe Leu Arg His Gln Cys Ser Pro Thr Ala Thr Pro Tyr Cys			
178	130	135	140	
179	Ser Pro Gln Cys Gln Ser Leu Arg Gln Gln Cys Cys Gln Gln Leu Arg			
180	145	150	155	160
181	Gln Val Glu Pro Gln His Arg Tyr Gln Ala Ile Phe Gly Leu Val Leu			
182	165	170	175	
183	Gln Ser Ile Leu Gln Gln Pro Gln Ser Gly Gln Val Ala Gly Leu			
184	180	185	190	
185	Leu Ala Ala Gln Ile Ala Gln Gln Leu Thr Ala Met Cys Gly Leu Gln			
186	195	200	205	
187	Gln Pro Thr Pro Cys Pro Tyr Ala Ala Ala Gly Gly Val Pro His			
188	210	215	220	

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Input Set : A:\50026.004001.SEQLIST.TXT
Output Set: N:\CRF3\04032002\I117246B.raw

191 <210> SEQ ID NO: 8
192 <211> LENGTH: 693
193 <212> TYPE: DNA
194 <213> ORGANISM: maize
196 <220> FEATURE:
197 <221> NAME/KEY: CDS
198 <222> LOCATION: (1)...(693)
200 <400> SEQUENCE: 8
201 atg agg gtg ttg ctc gcc ctc gct ctc ctg gct ctc gct gcg agc 48
202 Met Arg Val Leu Leu Val Ala Leu Ala Leu Ala Leu Ala Ala Ser
203 1 5 10 15
205 gcc acc tcc acg cat aca agc ggc ggc tgc ggc tgc cag cca ccg ccg 96
206 Ala Thr Ser Thr His Thr Ser Gly Gly Cys Gly Cys Gln Pro Pro Pro
207 20 25 30
209 ccg gtt cat cta ccg ccg ccg gtg cat ctg cca cct ccg gtt cac ctg 144
210 Pro Val His Leu Pro Pro Val His Leu Pro Pro Val His Leu
211 35 40 45
213 cca cct ccg gtg cat ctc cca ccg ccg gtc cac ctg ccg ccg ccg gtc 192
214 Pro Pro Pro Val His Leu Pro Pro Val His Leu Pro Pro Pro Val
215 50 55 60
217 cac ctg cca ccg ccg gtc cat gtg ccg ccg ccg gtt cat ctg ccg ccg 240
218 His Leu Pro Pro Pro Val His Val Pro Pro Pro Val His Leu Pro Pro
219 65 70 75 80
221 cca cca tgc cac tac cct act caa ccg ccc ccg atc gaa ttc aaa cca 288
222 Pro Pro Cys His Tyr Pro Thr Gln Pro Pro Arg Ile Glu Phe Lys Pro
223 85 90 95
225 aag cca aag ccg aag cca aaa gaa ttc aaa cca aag cca aag ccg aag 336
226 Lys Pro Lys Pro Lys Pro Lys Glu Phe Lys Pro Lys Pro Lys Pro Lys
227 100 105 110
229 cca aaa gaa ttc ctg cag ccc ctg cag gga acc tgc ggc gtt ggc agc 384
230 Pro Lys Glu Phe Leu Gln Pro Leu Gln Gly Thr Cys Gly Val Gly Ser
231 115 120 125
233 acc ccg atc ctg ggc cag tgc gtc gag ttt ctg agg cat cag tgc agc 432
234 Thr Pro Ile Leu Gly Gln Cys Val Glu Phe Leu Arg His Gln Cys Ser
235 130 135 140
237 ccg acg gcg acg ccc tac tgc tcc cct cag tgc cag tgc ttg ccg cag 480
238 Pro Thr Ala Thr Pro Tyr Cys Ser Pro Gln Cys Gln Ser Leu Arg Gln
239 145 150 155 160
241 cag tgt tgc cag ctc agg cag gtg gag ccg cag cac ccg tac cag 528
242 Gln Cys Cys Gln Gln Leu Arg Gln Val Glu Pro Gln His Arg Tyr Gln
243 165 170 175
245 gcg atc ttc ggc ttg gtc ctc cag tcc atc ctg cag cag cag ccg caa 576
246 Ala Ile Phe Gly Leu Val Leu Gln Ser Ile Leu Gln Gln Gln Pro Gln
247 180 185 190
249 agc ggc cag gtc gcg ggg ctg ttg gcg gcg cag ata gcg cag caa ctg 624
250 Ser Gly Gln Val Ala Gly Leu Leu Ala Ala Gln Ile Ala Gln Gln Leu
251 195 200 205
253 acg gcg atg tgc ggc ctg cag cag ccg act cca tgc ccc tac gct gct 672
254 Thr Ala Met Cys Gly Leu Gln Gln Pro Thr Pro Cys Pro Tyr Ala Ala

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255 210 215 220 693
 257 gcc ggc ggt gtc ccc cac tga
 258 Ala Gly Gly Val Pro His *
 259 225 230
 262 <210> SEQ ID NO: 9
 263 <211> LENGTH: 230
 264 <212> TYPE: PRT
 265 <213> ORGANISM: maize
 267 <400> SEQUENCE: 9
 268 Met Arg Val Leu Leu Val Ala Leu Ala Leu Ala Leu Ala Ala Ser
 269 1 5 10 15
 270 Ala Thr Ser Thr His Thr Ser Gly Gly Cys Gly Cys Gln Pro Pro Pro
 271 20 25 30
 272 Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu
 273 35 40 45
 274 Pro Pro Pro Val His Leu Pro Pro Pro Val His Leu Pro Pro Pro Val
 275 50 55 60
 276 His Leu Pro Pro Pro Val His Val Pro Pro Pro Val His Leu Pro Pro
 277 65 70 75 80
 278 Pro Pro Cys His Tyr Pro Thr Gln Pro Pro Arg Ile Glu Phe Lys Pro
 279 85 90 95
 280 Lys Pro Lys Pro Lys Pro Lys Glu Phe Lys Pro Lys Pro Lys Pro Lys
 281 100 105 110
 282 Pro Lys Glu Phe Leu Gln Pro Leu Gln Gly Thr Cys Gly Val Gly Ser
 283 115 120 125
 284 Thr Pro Ile Leu Gly Gln Cys Val Glu Phe Leu Arg His Gln Cys Ser
 285 130 135 140
 286 Pro Thr Ala Thr Pro Tyr Cys Ser Pro Gln Cys Gln Ser Leu Arg Gln
 287 145 150 155 160
 288 Gln Cys Cys Gln Gln Leu Arg Gln Val Glu Pro Gln His Arg Tyr Gln
 289 165 170 175
 290 Ala Ile Phe Gly Leu Val Leu Gln Ser Ile Leu Gln Gln Pro Gln
 291 180 185 190
 292 Ser Gly Gln Val Ala Gly Leu Leu Ala Ala Gln Ile Ala Gln Gln Leu
 293 195 200 205
 294 Thr Ala Met Cys Gly Leu Gln Gln Pro Thr Pro Cys Pro Tyr Ala Ala
 295 210 215 220
 296 Ala Gly Gly Val Pro His
 297 225 230
 300 <210> SEQ ID NO: 10
 301 <211> LENGTH: 723
 302 <212> TYPE: DNA
 303 <213> ORGANISM: Maize
 305 <220> FEATURE:
 306 <221> NAME/KEY: CDS
 307 <222> LOCATION: (1)...(723)
 309 <400> SEQUENCE: 10
 310 atg agg gtg ttg ctc gtt gcc ctc gct ctc ctg gct ctc gct gcg agc 48
 311 Met Arg Val Leu Leu Val Ala Leu Ala Leu Ala Leu Ala Ser

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